



SEQUENCE LISTING

<110> Clark, Janet

<120> METHOD FOR IDENTIFYING COMPOUNDS THAT  
AFFECT EXPRESSION OF TRYPTOPHAN HYDROXYLASE ISOFORM 2

<130> 21487YP

<140> 10/576,807

<141> 2006-04-21

<150> PCT/US2004/34619

<151> 2004-10-20

<150> 60/514,268

<151> 2003-10-24

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 447

<212> PRT

<213> Mus musculus

<400> 1

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1 5 10 15  
Glu Arg Gly Arg Val Thr Leu Ile Phe Ser Leu Glu Asn Glu Val Gly  
20 25 30  
Gly Leu Ile Lys Val Leu Lys Ile Phe Gln Glu Asn His Val Ser Leu  
35 40 45  
Leu His Ile Glu Ser Arg Lys Ser Lys Gln Arg Asn Ser Glu Phe Glu

50	55	60
Ile Phe Val Asp Cys Asp	Ile Ser Arg Glu Gln Leu Asn Asp	Ile Phe
65	70	75 80
Pro Leu Leu Lys Ser His Ala Thr Val Leu Ser Val Asp Ser Pro Asp		
85	90	95
Gln Leu Thr Ala Lys Glu Asp Val Met Glu Thr Val Pro Trp Phe Pro		
100	105	110
Lys Lys Ile Ser Asp Leu Asp Phe Cys Ala Asn Arg Val Leu Leu Tyr		
115	120	125
Gly Ser Glu Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr		
130	135	140
Arg Arg Arg Arg Lys Tyr Phe Ala Glu Leu Ala Met Asn Tyr Lys His		
145	150	155 160
Gly Asp Pro Ile Pro Lys Ile Glu Phe Thr Glu Glu Glu Ile Lys Thr		
165	170	175
Trp Gly Thr Ile Phe Arg Glu Leu Asn Lys Leu Tyr Pro Thr His Ala		
180	185	190
Cys Arg Glu Tyr Leu Arg Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly		
195	200	205
Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu		
210	215	220
Lys Glu Arg Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser		
225	230	235 240
Pro Arg Asp Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr		
245	250	255
Gln Tyr Val Arg His Ser Ser Asp Pro Leu Tyr Thr Pro Glu Pro Asp		
260	265	270
Thr Cys His Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser		
275	280	285
Phe Ala Gln Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser		
290	295	300
Glu Glu Thr Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu		
305	310	315 320
Phe Gly Leu Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly		
325	330	335
Leu Leu Ser Ser Ile Ser Glu Leu Lys His Ala Leu Ser Gly His Ala		
340	345	350

Lys Val Lys Pro Phe Asp Pro Lys Ile Ala Cys Lys Gln Glu Cys Leu  
 355 360 365  
 Ile Thr Ser Phe Gln Asp Val Tyr Phe Val Ser Glu Ser Phe Glu Asp  
 370 375 380  
 Ala Lys Glu Lys Met Arg Glu Phe Ala Lys Thr Val Lys Arg Pro Phe  
 385 390 395 400  
 Gly Leu Lys Tyr Asn Pro Tyr Thr Gln Ser Val Gln Val Leu Arg Asp  
 405 410 415  
 Thr Lys Ser Ile Thr Ser Ala Met Asn Glu Leu Arg Tyr Asp Leu Asp  
 420 425 430  
 Val Ile Ser Asp Ala Leu Ala Arg Val Thr Arg Trp Pro Ser Val  
 435 440 445

<210> 2

<211> 488

<212> PRT

<213> Mus musculus

<400> 2

Met Gln Pro Ala Met Met Met Phe Ser Ser Lys Tyr Trp Ala Arg Arg  
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 20 25 30  
 Ser Leu Thr Gln Asn Lys Ala Ile Lys Ser Glu Asp Lys Lys Ser Gly  
 35 40 45  
 Lys Glu Pro Gly Lys Gly Asp Thr Thr Glu Ser Ser Lys Thr Ala Val  
 50 55 60  
 Val Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Val Lys Ala Leu Arg  
 65 70 75 80  
 Leu Phe Gln Glu Lys His Val Asn Met Leu His Ile Glu Ser Arg Arg  
 85 90 95  
 Ser Arg Arg Arg Ser Ser Glu Val Glu Ile Phe Val Asp Cys Glu Cys  
 100 105 110  
 Gly Lys Thr Glu Phe Asn Glu Leu Ile Gln Leu Leu Lys Phe Gln Thr  
 115 120 125  
 Thr Ile Val Thr Leu Asn Pro Pro Glu Ser Ile Trp Thr Glu Glu Glu

130	135	140
Asp Leu Glu Asp Val Pro Trp Phe Pro Arg Lys Ile Ser Glu Leu Asp		
145	150	155
Arg Cys Ser His Arg Val Leu Met Tyr Gly Thr Glu Leu Asp Ala Asp		
165	170	175
His Pro Gly Phe Lys Asp Asn Val Tyr Arg Gln Arg Arg Lys Tyr Phe		
180	185	190
Val Asp Val Ala Met Gly Tyr Lys Tyr Gly Gln Pro Ile Pro Arg Val		
195	200	205
Glu Tyr Thr Glu Glu Glu Thr Lys Thr Trp Gly Val Val Phe Arg Glu		
210	215	220
Leu Ser Lys Leu Tyr Pro Thr His Ala Cys Arg Glu Tyr Leu Lys Asn		
225	230	235
Leu Pro Leu Leu Thr Lys Tyr Cys Gly Tyr Arg Glu Asp Asn Val Pro		
245	250	255
Gln Leu Glu Asp Val Ser Met Phe Leu Lys Glu Arg Ser Gly Phe Thr		
260	265	270
Val Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp Phe Leu Ala Gly		
275	280	285
Leu Ala Tyr Arg Val Phe His Cys Thr Gln Tyr Val Arg His Gly Ser		
290	295	300
Asp Pro Leu Tyr Thr Pro Glu Pro Asp Thr Cys His Glu Leu Leu Gly		
305	310	315
His Val Pro Leu Leu Ala Asp Pro Lys Phe Ala Gln Phe Ser Gln Glu		
325	330	335
Ile Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Asp Val Gln Lys Leu		
340	345	350
Ala Thr Cys Tyr Phe Phe Thr Ile Glu Phe Gly Leu Cys Lys Gln Glu		
355	360	365
Gly Gln Leu Arg Ala Tyr Gly Ala Gly Leu Leu Ser Ser Ile Gly Glu		
370	375	380
Leu Lys His Ala Leu Ser Asp Lys Ala Cys Val Lys Ser Phe Asp Pro		
385	390	395
Lys Thr Thr Cys Leu Gln Glu Cys Leu Ile Thr Thr Phe Gln Asp Ala		
405	410	415
Tyr Phe Val Ser Asp Ser Phe Glu Glu Ala Lys Glu Lys Met Arg Asp		
420	425	430

Phe Ala Lys Ser Ile Thr Arg Pro Phe Ser Val Tyr Phe Asn Arg Tyr  
435 440 445  
Thr Gln Ser Ile Glu Ile Leu Lys Asp Thr Arg Ser Ile Glu Asn Val  
450 455 460  
Val Gln Asp Leu Arg Ser Asp Leu Asn Thr Val Cys Asp Ala Leu Asn  
465 470 475 480  
Lys Met Asn Gln Tyr Leu Gly Ile  
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<212> DNA  
<213> Artificial Sequence

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<223> TPH2a riboprobe template

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atcaaaagcg aggacaagaa aagcggcaaa gagcccggca aaggcgacac cacagagagc 180  
agcaagacag cagttgtgtt ctccttgaag aatgaagtt 219

<210> 4  
<211> 219  
<212> DNA  
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<220>  
<223> TPH2b riboprobe

<400> 4  
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cgggtcccggc gaagaagttc tgaagtcgaa atcttcgtgg actgcgaatg tggcaaaacg 120  
gaattcaatg agctcatcca gttgctgaaa tttcagacca ccattgtgac cctgaatccg 180  
cctgagagca tttggacgga ggaagaagat ctcgaggat 219

<210> 5

<211> 818

<212> DNA

<213> Artificial Sequence

<220>

<223> TPH2c riboprobe

<400> 5

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aaaagcgagg acaagaaaag cggcaaagag cccggcaaag gcgacaccac agagagcagc 180
aagacagcag ttgtgttctc cttgaagaat gaagttggtg ggctggtgaa agcacttaga 240
ctattccagg aaaaacatgt caacatgctt catatcgaat ccaggcggtc ccggcgaaga 300
agtttctaagt cgaaatcttc gtggactgcg aatgtggcaa aacggaattc aatgagctca 360
tccagttgct gaaatctcag accaccattg tgaccctgaa tccgcctgag agcatttgga 420
cggaggaaga agatctcgag gatgtgccgt ggttcctctg gaagatctct gagttagaca 480
gatgctctca ccgagtcctc atgtacggca ccgagcttga tgccgaccat ccaggattta 540
aggacaatgt ctatcgacag aggaggaagt attttgtgga tgtggccatg ggctataaat 600
atggtcagcc cattcccagg gtcgagtaca cagaagaaga gactaaaact tggggtgttg 660
tgttcgagg gctctccaaa ctctaccga ctcattgctt ccgggagtag ctgaaaaacc 720
tccccctgct gaccaagtac tgtggctaca ggggaagacaa cgtgccgcaa ctggaagacg 780
tctccatgtt tctgaaagag cgatctggct tcacagtg 818
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<212> DNA

<213> Artificial Sequence

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<223> TPH2-892 riboprobe

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tacccgaccc acgctgcag ggagtacctc agaaacctcc ctttgctctc aaaatactgt 120
ggctatcggg aagacaacat cccgcaactg gaggatgtct ccaacttttt aaaagaacgc 180
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actggggtttt ccatccgtcc tgtggctggg tacctctcac cgagagattt tctgtcgggg 240  
 ttagcctttc gagtctttca ctgcactcag tatgtgagac acagttcaga tccccctctac 300  
 actccagagc cagacacctg ccatgaactc ctaggccaag ttcctctctt ggctgaaccc 360  
 agttttgtct aattctccca agaaattggc ctggcttccc ttggagcttc agaggagaca 420  
 gttcaaaaac tggcaacgtg ctactttttc actgtggagt ttgggctgtg caaacaagat 480  
 ggacagctga gagtcttttg ggccggcttg ctttcttcca tcagtgaact caaacatgca 540  
 ctttctggac atgccaaaagt caagcccttt gatcccaaga ttgcctgtaa acaggaatgt 600  
 ctcacacga gcttccagga tgtctacttt gtatctgaga gctttgaaga tgcaaaggag 660  
 aagatgagag aatttgccaa gaccgtgaag cgcccgtttg gactgaagta caaccgtac 720  
 acacagagtg ttcaggttct cagagacacc aagagcataa ctagtgccat gaatgagttg 780  
 cggtagacct tgatgtcatc agtgatgcc tgcctagggt caccaggtgg cccagtgtgt 840  
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<211> 22

<212> DNA

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<223> Murine TPH2 forward primer mTPH2-514F

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<210> 8

<211> 21

<212> DNA

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<400> 8

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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Murine TPH2 reverse primer mTPH2-585R

<400> 9

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22

<210> 10

<211> 21

<212> DNA

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<223> Murine TPH2 reverse primer mTPH2-1344R

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21

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Murine TPH2 probe mTPH2-565T

<400> 11

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27

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Murine TPH2 probe mTPH2-1292T

<400> 12

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26